

alignment_block:

US-09-525-998a-1 x WSL1_HUMAN

Align seq 1/1 to: WSL1_HUMAN from: 1 to: 417

```

43 CTCGTGAGACTGTGGTGGGAATAATACGCTCAGAGGTTTATGAGACTGTT 92
15 LeuLeuLeuValLeuLeuGlyAlaProAlaGlyGly 26
93 CCTTCACCTACGACGACAGACAGACATAGTGTGTGTCGCCCAAGGAA 142
27 GlyThrArgSerProArg 37
143 AATATATGACGCTCAAAATTAATGATGATGATGATGATGATGATGATGAT 192
37 TyaspPheHisTysTysTysTysTysTysTysTysTysTysTysTysTys 53
193 GGAACCTACTTGTATATATATATATATATATATATATATATATATATAT 242
54 GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCys 70
243 CAGGACGTCGTGACAGGCGCTGCTTCACGCTGCTTCACGCTGCTTCACG 291
70 sLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisHisAsnS 87
292 CACTGCTCTATATATATATATATATATATATATATATATATATATATAT 349
87 cLeuCysAlaAlaCysSerAlaCysAspGluGlnAlaSerGlnAlaAla 103
340 ATCTCTCTTTCATAGTATATATATATATATATATATATATATATATATAT 389
104 LeuGlnAsnTyrSerAlaValAlaAspThrArgCysGlyTyrGlySProG 120
390 GCACACGCGCATATATATATATATATATATATATATATATATATATATAT 429
120 TyrPheValGlnCys 134
430 TTTCAATTTACGCTGCTCTCAAT 465
134 crProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHis 150
466 CTCTCTCTGACAGGAAACAAACAAACAAACAAACAAACAAACAAACAAAC 509
151 ThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThrCysLeuPr 167
510 AGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
167 cGlyPheTyrGlnHisGlyAspGlyCysValSerCysPheThrSerThrL 184
547 AGTAAGTGTAAATAAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 594
184 euGlySerCysProGlu 195
595 ATTGAGAAATGTAAGGCACTGAGGACATCAAGGACATCAAGGACATCAAG 644
196 231
645 CTCTGTCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 694
203 LglValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrL 220
695 TAATGATATGCTACCAAGG...TGAAGATGCAAGGCTACTACTGCTTGT 741
220 euThrTyrThrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 231
742 TGTGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 791
232 ProLeuValThrAlaAlaAspAlaGlyMetGluAlaLeuThrPr 246
792 TAAGGCG 832
246 oProProAlaThrHisLeuSerProLeuAspSer 257

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833 GCTTCATACCAAGATGGAGTTCAGTATGATGATGATGATGATGATGATGAT 882
258 AlaHisThrLeuLeuAlaProProAspSerSerThrLysTyrCys 272
883 TCC 909
273 ThrValGlnLeuValGlnTyrAspSerTyrPheGlnTyrPheGlnTyrP 289
910 TGTCCCAACTTTGCG 944
289 nGluAlaLeuLeuCysProThrValThrTrpSerTrpAspGlnLeuProSer 406
935 GAGAGGTGGACACACGCTATATAGAGGGGCTGAGGCAATGCTTGGACAG 484
306 rGluAlaLeuGlyPro 410
985 CTCCGCTCCGACGACCAATCCCAACCCGCTTCAGAAAGTCCGACACACAG 1044
311 AlaAlaAlaProThrLeuSerPro 1022
1035 CCACACGACACACAGCCTACACACCTGACACCTGACACCTGACACCTGAC 1084
322 acGlySerProAlaMetMetLeuGlnProGlyPro 1084
1085 TGGTGAATAAGTGGCGGCTGGTGGCGGCTGGTGGCGGCTGGTGGCGGCTG 1144
338 alMetAspAlaValProAlaTrpArgTrpLysGlnPheValArgThrLeu 454
1135 GCGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1184
355 GlyLeuAlaGlnAlaGlnLeuGlnAlaValGlnAlaValGlnAlaValG 479
1185 GCTGGCGGACGCGCAATACAGATACGCGGACGCGCAATACAGCGCGGAC 1234
371 PheArgAspGlnGlnTyrGlnMetLeuTyrArgTrpArgGlnGlnGln 487
1235 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1284
387 Phe 1323
1285 GACCTGCTGCGCTGCGCTGCGGACGACGACGACGACGACGACGACGACG 1323
401 GlyLeuAspGlyCysValGlnAspLeuArgSerAlaVal 415
seq.name: SwissProt_39:INMC_HUMAN
seq.documentation_block:
ID THRC_HUMAN STANDARD: PRT: 435 AA.
AC P36941;
DT 01-JUN-1994 (rel. 29, created)
DT 01-JUN-1994 (rel. 29, last sequence update)
DE LYMPHOXIN-BETA RECEPTOR PRECURSOR (LIMPH NECROSIS FACTOR RECEPTOR)
DE 2 RELATED PROTEIN (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTR OR TRNK OR INTRNS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE:94252481; PubMed:8486360;
FA Klags M., Stadler M., Ditsman J., de Mele H., Maryon P.;
RI "Construction and evaluation of a human library of human ltr
PL transcribed sequences derived from a genomic cell hybrid."
RN [2]
RP FUNCTION.
RX MEDLINE:94252499; PubMed:8471423;
RA Crowe P.D., Van Arsdale P.L., Walter R.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Bin W.S., Goodwin R.G., Smith C.A.;
RI "A lymphotoxin beta specific receptor."

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343 hrGlyGlySerValThrValThrGlyAsnIlePylIleTyrAsnGlyPro 359
953 ATCAAGAGGAGTGAAC.....ACATAGATTAGACACAGGAGGAGTCAAGAC 996
360 ValLeuGlyGlyThrArgGlyProGly AspProProAlaIleProGlyGly 375
997 CCCATCC.....CCACGCCCTTCACAAATTCGATACACAGGCGCCCAAGCC 1043
375 uProProTyrProThrPro.....GlyGlyGlyAlaProGlyProSerGly 390
1044 ACACAGGCTACACATACACACAGCCCG 1069
391 .....LeuSerThrPro 394
seq_name: SwissProt_49:NGFR_RAT
seq_documentation_block:
ID NCGRF_RAT STANJARD: PRT: 425 AA.
AC P07174:
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 20-AUG-2001 (Rel. 43, Last annotation update)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-NGFR) (p75 NCD)
DE NCGRF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCHI_TaxID-10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE-87115859; PubMed-3027580;
RA Radeke M.J., Misko T.P., Iisu C., Herzenberg L.A., Shooter E.M.;
RT "Gene transfer and molecular cloning of the rat nerve growth factor receptor."
RL Nature 325:593-597(1987).
RL Nature 325:593-597(1987).
RN [2]
SEQUENCE OF 1-22 FROM N.A.
RX TISSUE-Liver;
RX MEDLINE-93077038; PubMed-1446821;
RA Metcalf M., Timmusk T., Allikmets R., Saarman M., Persson H.;
RT "Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter."
RL Gene 121:247-254(1992).
RN [3]
STRUCTURE BY NMR OF 334-418.
RX MEDLINE-97449145; PubMed-9305641;
RA Liepinsh E., Ilag L.L., Otting G., Ibanes C.F.;
RT "NMR structure of the death domain of the p75 neurotrophin receptor."
RL EMBO J. 16:4999-5005(1997).
CC [1] FUNCTION: LOW AFFINITY PEPTIDE WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC [2] SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC [3] SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC [4] PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC [5] SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION.
CC [6] SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch)
CC
CC EMBL: X05137; CAA28783.1.
CC EMBL: X61269; NOT_ANNOTATED_CDS.
CC PIR: A26431; A26431
CC DOI: 1NGR; 29-JUL-97.
CC InterPro: IPR000448; death
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 425 LOW AFFINITY NERVE GROWTH FACTOR
FT RECEPTOR.
FT DOMAIN 30 251 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 252 273 POTENTIAL.
FT DOMAIN 274 425 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 190 4 X TNFR-CYS.
FT REPEAT 32 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT REPEAT 109 148 TNFR-CYS 3.
FT REPEAT 149 190 TNFR-CYS 4.
FT DOMAIN 198 249 SER/THR-RICH.
FT DOMAIN 354 419 DEATH.
FT DISULFID 33 44 BY SIMILARITY.
FT DISULFID 45 58 BY SIMILARITY.
FT DISULFID 48 65 BY SIMILARITY.
FT DISULFID 68 84 BY SIMILARITY.
FT DISULFID 87 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT DISULFID 110 123 BY SIMILARITY.
FT DISULFID 126 139 BY SIMILARITY.
FT DISULFID 129 147 BY SIMILARITY.
FT DISULFID 150 165 BY SIMILARITY.
FT DISULFID 168 181 BY SIMILARITY.
FT DISULFID 171 189 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SPOURCE 425 AA; 45432 MW; R2E15293D3827F8 CRC64,
alignment_scores:
Quality: 424.00 Length: 495
Ratio: 1.057 Gaps: 27
Percent Similarity: 42.626 Percent Identity: 23.232
alignment_block:
US-09-525-998A-1 x NGFR_RAT
Align seq 1/1 LO: NGFR_RAT from: 1 to: 425
40 GTAATATGAGATTTTGTGGAGATATACCCCTGAGGGGTTATTGGACT 89
16 LeuLeuLeuLeuLeuLeuLeuValSerSerGlyGlyAla..... 29
90 GCTGCTTCATCTAGGGGACACAGGACAGACAGATAGTGTGTCTCCCAAG 139
30 ..... 139
140 GAATAATATATATATATATATATATATATATATATATATATATATATAT 189
36 LysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 49
190 AAGAGATATATATATATATATATATATATATATATATATATATATATAT 239
50 LeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 64
240 CACACAGGCTACACATACACAGCCCGTTCACACACACACACACACAC 286
64 LysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 81
287 TCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 336
81 ArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 94

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DOMAIN	27	186	4 X TNFR-CYS
FT	27	186	
REPEAT	27	62	TNFR-CYS 1
FT	63	104	TNFR-CYS 2
REPEAT	63	104	
FT	105	147	TNFR-CYS 3
REPEAT	105	147	
FT	148	186	TNFR-CYS 4
REPEAT	148	186	
CARBOHYD	66	66	N-LINKED (GLCNAC...) (POTENTIAL)
FT	181	181	N-LINKED (GLCNAC...) (POTENTIAL)
FT	205	205	N-LINKED (GLCNAC...) (POTENTIAL)
FT	238	238	N-LINKED (GLCNAC...) (POTENTIAL)
CARBOHYD	238	238	N-LINKED (GLCNAC...) (POTENTIAL)
SEQUENCE	535	535	AA: 535-538 MW: 48602.274 Da pI: 6.0634


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816 CTTAGTGGGACTGACAGGCTTCACGCGGACGCTGGGCTTCAGT..... 858
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
193 uV41111etysThryscLupheThrValThrLCSAsnTyThrAspCysA 210

859 ..CGAGTGGCGAGTGGACGCTTCACGCGGACGCTCC 891
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
210 sPpovAlPheHisThrGlutTyTyrAlaThrSer 221

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